EXHIBIT A

A MARKED UP VERSION OF THE AMENDED PARAGRAPHS IN THE SPECIFICATION FILED ON JUNE 18, 2002 IN U.S. APPLICATION SERIAL NO.: 09/610,118 ATTORNEY DOCKET NO.: 7853-211

On page 1, please amend the paragraph beginning on line 3 as follows:

This application is a continuation-in-part of U.S. Application Serial No. 09/503,387, filed February 14, 2000, which is a continuation-in-part of U.S. Application Serial No. 09/454,824, filed December 6, 1999, which is a continuation-in-part of U.S. Application Serial No. [09/345,068] 09/345,468, filed June 30, 1999, the entire contents of each of which is incorporated herein by reference its entirety.

On page 14, please amend the paragraph beginning on line 25 as follows:

FIGURES [3A-3D] 3A-3C depict an alignment of the nucleotide sequence of the open reading frame for human monocyte inhibitory receptor precursor (SEQ ID NO:24; GenBank Accession Number U91928) and the nucleotide sequence of the open reading frame for human TANGO 268 (SEQ ID NO:2). The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and human TANGO 268 are 37.7% identical. The nucleotide sequences of full-length, including the 5' and 3' untranslated regions (UTRs), human monocyte inhibitory receptor precursor SEQ ID NO:11; GenBank Accession Number U91928) and human TANGO 268 are 49.9% identical. These alignments were performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 14, please amend the paragraph beginning on line 35 as follows:

[FIGURES 4A-4B depict] FIGURE 4 depicts an alignment of the amino acid sequence of human monocyte inhibitory receptor precursor (SEQ ID NO:12) and the amino acid sequence of human TANGO 268 (SEQ ID NO:3). The amino acid sequences of human monocyte inhibitory receptor precursor and human TANGO 268 are 23.0% identical. This alignment was performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 16, please amend the paragraph beginning on line 1 as follows:

[FIGURES 9A-9B depict] FIGURE 9 depicts an alignment of the amino acid sequence of human monocyte inhibitory receptor precursor (SEQ ID NO:12) and the amino acid sequence of mouse TANGO 268 (SEQ ID NO:16). The amino acid sequences of human monocyte inhibitory receptor precursor and mouse TANGO 268 are 20.3% identical. This alignment was performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 19, please amend the paragraph beginning on line 24 as follows:

[FIGURE 25] FIGURES 25A-25I: FACS analysis of the seven unique scFv's. Purified scFv's were incubated with U937 cells expressing GPVI (GPVI-U937 cells) and the binding of scFv's to GPVI-U937 cells was detected by FACS analysis.

On page 27, please amend the paragraph beginning on line 10 as follows:

Figures [3A-3D] 3A-3C show an alignment of the human TANGO 268 coding region (SEQ ID NO:2) with the human monocyte inhibitory receptor precursor protein coding region (SEQ ID NO:24). The human monocyte inhibitory receptor has been shown to downregulate activation responses by phosphatases. The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and human TANGO 268 are 37.7% identical. The full-length nucleic acid sequence of human TANGO 268 (SEQ ID NO:1) exhibits 49.9% identity to the full-length nucleic acid human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928).

On page 27, please amend the paragraph beginning on line 18 as follows:

[Figures 4A-4B show] Figure 4 shows that there is an overall 23% identity between the amino acid sequence of the human TANGO 268 protein and the amino acid sequence of the human monocyte inhibitory receptor protein (SEQ ID NO:12; Accession Number U91928).

On page 30, please amend the paragraph beginning on line 9 as follows:

In general, mouse TANGO 268 has most homology to various members of the immunoglobulin superfamily that includes NK inhibitory and activating receptors and Fc receptors. The full-length nucleic acid sequence of mouse TANGO 268 exhibits 35.6%

identity to the full-length nucleic acid human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928). Figures 8A-8B show an alignment of the mouse TANGO 268 coding region (SEQ ID NO:15) with the human monocyte inhibitory receptor precursor protein coding region (SEQ ID NO:24). The nucleotide sequences of the coding regions of human monocyte inhibitory receptor precursor and mouse TANGO 268 are 34.4% identical. The nucleotide sequences of the full-length human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928) and full-length mouse TANGO 268 (SEQ ID NO:14) are 35.6% identical. [Figures 9A-9B show] Figure 9 shows that there is an overall 20.3% identity between the mouse TANGO 268 amino acid sequence and the human monocyte inhibitory receptor protein amino acid sequence (SEQ ID NO:12; Accession Number U91928).

On page 54, please amend the paragraph beginning on line 31 as follows:

Microtiter plates (ImmulonII Dynex) were coated with type I or type III collagen (40 µg/mL in 20 mM CH_3COOH) overnight at 4°C and then saturated with 2 mg/mL BSA for two hours at room temperature. [Solube] Soluble human GPVI-Fc (5 nM in PBS pH 7.4 containing 0.2% BSA and 0.1 % Tween) in the absence or the presence of [antibobies] antibodies (10 µg/mL) was added to the wells of the microtiter plate and the plates were incubated for two hours at room temperature. After washing the wells, peroxidase coupled protein A (Amersham) was added to the wells and the plates were incubated for 2 hours at room temperature. After washing, peroxidase substrate was added and OD was measured at 495 nm.

On page 55, please amend the paragraph beginning on line 3 as follows:

Microtiter plates (ImmulonII Dynex) were coated with monoclonal antibody 1P10.2 (5 µg/mL in PBS) overnight at 4°C and then saturated with 2 mg/mL BSA two hours at room temperature. [Solube] Soluble human GPVI-Fc (0.5 nM in PBS pH 7.4 containing 0.2% BSA and 0.1 % tween) was added to the wells of the plate and the plate was incubated for two hours at room temperature. After washing the wells, buffer or antibodies (10 µg/mL) were added to the wells and the plates were incubated for one hour at room temperature. Next, ^{125}I-labeled convulxin (~1 nM) was added to the wells and the plates were incubated for approximately 10 minutes. The wells were washed and counted for ^{125}I-convulxin binding in a gamma counter.

On page 56, please amend the paragraph beginning on line 1 as follows:

Bst NI fingerprinting of the 28 positive clones is shown in Figure 24. A total of seven unique clones were found of the pool. All of seven of the clones recognized GPVI on transduced cells in a FACS experiment ([Figure 25] Figures 25A-25I). CDR sequences of scFvs are shown in Table 7 below.